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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/09/882,986

TIME: 14:51:14

Input Set : A:\-12-1.app

Output Set: N:\CRF3\01282002\I882986.raw

ENTERED

3 <110> APPLICANT: Schroeder, Julian
 4 Hugouvieux, Veronique
 5 Kwak, June M.
 6 The Regents of the University of California
 8 <120> TITLE OF INVENTION: Modulation of Absciscic Acid Signal Transduction in
 9 Plants
 11 <130> FILE REFERENCE: 19452A-001210US
 13 <140> CURRENT APPLICATION NUMBER: US 09/882,986
 14 <141> CURRENT FILING DATE: 2001-06-14
 16 <150> PRIOR APPLICATION NUMBER: US 60/212,068
 17 <151> PRIOR FILING DATE: 2000-06-14
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2716
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Arabidopsis thaliana
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: abscisic acid (ABA) hypersensitive (ABH1) cDNA
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (37)..(2583)
 34 <223> OTHER INFORMATION: ABH1 protein
 36 <400> SEQUENCE: 1
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 39 gagacttggt tcggtgtcat tcgtagagaa atcgagcggt ctggagatca agttttgcct 180
 40 tttctactac aatgtgctga acaattgcct cataagattc ctttgtatgg gactttgatt 240
 41 ggtttgttga acttggagaa tgaagatttt gtccagaagc tagtagaaag tgtccacgct 300
 42 aatttccagg tcgctttaga ttctggcaac tgcaacagta tccgtatatt gcttcgcttt 360
 43 atgacttccc tgttgtgcag taagggttatt caacctgctt ctttgattgt cgtcttcgaa 420
 44 acattgctat catctgctgc cactactgtg gatgaagaga aaggaaatcc atcatggcag 480
 45 ccacaagctg acttttacgt tatatgcac ttgtccagcc tcccgtgggg aggatcagaa 540
 46 ctgctgagc aagttcctga tgagattgaa agagtgttag ttgggataca agcttatttg 600
 47 agcatccgaa agaattcttc cacctctggg ttaaactttt ttcacaacgg agaatttgaa 660
 48 agcagccttg cagagaagga tttcgtggag gatctattgg atcgaattca gtctctggct 720
 49 tccaatggat ggaaacttga aagcgtacac aggcctcacc tctcgtttga agctcaactc 780
 50 gttgctggaa agtttcatga gctacgtccc attaaatgta tggaaacaacc gactccacct 840
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 52 cagagaattc gtagggttga tatatttcca gctaataaaa tggaggatgt acaaccaatt 960
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56 tatacactcg tgattatgga tctttgtaag gctcttccgg gtgcctttcc tgctgttggt 1200
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58 cgtcttatcc tctggttttc tcaaccactta tccaacttcc aattcatctg gccgtgggaa 1320
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60 attttgcaaa gagaagtacg cttgtcttac tgggataaaa ttaagcagag cattgagaat 1440
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62 gaagaaggtg aagagaaaaac agaagaacag caattgtcag ccgaattgag caggaaggtc 1560
63 aaggaaaaac aaaccgcacg tgacatgata gtgtggattg aagaaacgat atatccagtt 1620
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85 <210> SEQ ID NO: 2

86 <211> LENGTH: 848

87 <212> TYPE: PRT

88 <213> ORGANISM: Arabidopsis thaliana

90 <220> FEATURE:

91 <223> OTHER INFORMATION: ABH1

93 <400> SEQUENCE: 2

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97           20           25           30
98 Gly Val Ile Arg Arg Glu Ile Glu Arg Ser Gly Asp Gln Val Leu Pro
99           35           40           45
100 Phe Leu Leu Gln Cys Ala Glu Gln Leu Pro His Lys Ile Pro Leu Tyr
101           50           55           60
102 Gly Thr Leu Ile Gly Leu Asn Leu Glu Asn Glu Asp Phe Val Gln
103           65           70           75           80
104 Lys Leu Val Glu Ser Val His Ala Asn Phe Gln Val Ala Leu Asp Ser
105           85           90           95
106 Gly Asn Cys Asn Ser Ile Arg Ile Leu Leu Arg Phe Met Thr Ser Leu
107           100          105          110
108 Leu Cys Ser Lys Val Ile Gln Pro Ala Ser Leu Ile Val Val Phe Glu

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109          115          120          125
110 Thr Leu Leu Ser Ser Ala Ala Thr Thr Val Asp Glu Glu Lys Gly Asn
111          130          135          140
112 Pro Ser Trp Gln Pro Gln Ala Asp Phe Tyr Val Ile Cys Ile Leu Ser
113 145          150          155          160
114 Ser Leu Pro Trp Gly Gly Ser Glu Leu Ala Glu Gln Val Pro Asp Glu
115          165          170          175
116 Ile Glu Arg Val Leu Val Gly Ile Gln Ala Tyr Leu Ser Ile Arg Lys
117          180          185          190
118 Asn Ser Ser Thr Ser Gly Leu Asn Phe Phe His Asn Gly Glu Phe Glu
119          195          200          205
120 Ser Ser Leu Ala Glu Lys Asp Phe Val Glu Asp Leu Leu Asp Arg Ile
121          210          215          220
122 Gln Ser Leu Ala Ser Asn Gly Trp Lys Leu Glu Ser Val Pro Arg Pro
123 225          230          235          240
124 His Leu Ser Phe Glu Ala Gln Leu Val Ala Gly Lys Phe His Glu Leu
125          245          250          255
126 Arg Pro Ile Lys Cys Met Glu Gln Pro Ser Pro Pro Ser Asp His Ser
127          260          265          270
128 Arg Ala Tyr Ser Gly Lys Gln Lys His Asp Ala Leu Thr Arg Tyr Pro
129          275          280          285
130 Gln Arg Ile Arg Arg Leu Asn Ile Phe Pro Ala Asn Lys Met Glu Asp
131          290          295          300
132 Val Gln Pro Ile Asp Arg Phe Val Val Glu Glu Tyr Leu Leu Asp Val
133 305          310          315          320
134 Leu Phe Tyr Leu Asn Gly Cys Arg Lys Glu Cys Ala Ser Tyr Met Ala
135          325          330          335
136 Asn Leu Pro Val Thr Phe Arg Tyr Glu Tyr Leu Met Ala Glu Thr Leu
137          340          345          350
138 Phe Ser Gln Ile Leu Leu Leu Pro Gln Pro Pro Phe Lys Thr Leu Tyr
139          355          360          365
140 Tyr Thr Leu Val Ile Met Asp Leu Cys Lys Ala Leu Pro Gly Ala Phe
141          370          375          380
142 Pro Ala Val Val Ala Gly Ala Val Arg Ala Leu Phe Glu Lys Ile Ser
143 385          390          395          400
144 Asp Leu Asp Met Glu Ser Arg Thr Arg Leu Ile Leu Trp Phe Ser His
145          405          410          415
146 His Leu Ser Asn Phe Gln Phe Ile Trp Pro Trp Glu Glu Trp Ala Phe
147          420          425          430
148 Val Leu Asp Leu Pro Lys Trp Ala Pro Lys Arg Val Phe Val Gln Glu
149          435          440          445
150 Ile Leu Gln Arg Glu Val Arg Leu Ser Tyr Trp Asp Lys Ile Lys Gln
151          450          455          460
152 Ser Ile Glu Asn Ala Thr Ala Leu Glu Glu Leu Leu Pro Pro Lys Ala
153 465          470          475          480
154 Gly Pro Asn Phe Met Tyr Ser Leu Glu Glu Gly Lys Glu Lys Thr Glu
155          485          490          495
156 Glu Gln Gln Leu Ser Ala Glu Leu Ser Arg Lys Val Lys Glu Lys Gln
157          500          505          510

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158 Thr Ala Arg Asp Met Ile Val Trp Ile Glu Glu Thr Ile Tyr Pro Val
159          515          520          525
160 His Gly Phe Glu Val Thr Leu Thr Ile Val Val Gln Thr Leu Leu Asp
161      530          535          540
162 Ile Gly Ser Lys Ser Phe Thr His Leu Val Thr Val Leu Glu Arg Tyr
163 545          550          555          560
164 Gly Gln Val Phe Ser Lys Leu Cys Pro Asp Asn Asp Lys Gln Val Met
165          565          570          575
166 Leu Leu Ser Gln Val Ser Thr Tyr Trp Lys Asn Asn Val Gln Met Thr
167          580          585          590
168 Ala Val Ala Ile Asp Arg Met Met Gly Tyr Arg Leu Val Ser Asn Gln
169      595          600          605
170 Ala Ile Val Arg Trp Val Phe Ser Pro Glu Asn Val Asp Gln Phe His
171      610          615          620
172 Val Ser Asp Gln Pro Trp Glu Ile Leu Gly Asn Ala Leu Asn Lys Thr
173 625          630          635          640
174 Tyr Asn Arg Ile Ser Asp Leu Arg Lys Asp Ile Ser Asn Ile Thr Lys
175          645          650          655
176 Asn Val Leu Val Ala Glu Lys Ala Ser Ala Asn Ala Arg Val Glu Leu
177          660          665          670
178 Glu Ala Ala Glu Ser Lys Leu Ser Leu Val Glu Gly Glu Pro Val Leu
179      675          680          685
180 Gly Glu Asn Pro Ala Lys Met Lys Arg Leu Lys Ser Thr Val Glu Lys
181      690          695          700
182 Thr Gly Glu Ala Glu Leu Ser Leu Arg Glu Ser Leu Glu Ala Lys Glu
183 705          710          715          720
184 Ala Leu Leu Asn Arg Ala Leu Ser Glu Thr Glu Val Leu Leu Leu Leu
185          725          730          735
186 Leu Phe Gln Ser Phe Leu Gly Val Leu Lys Glu Arg Leu Pro Asp Pro
187          740          745          750
188 Thr Lys Val Arg Ser Val Gln Asp Leu Lys Ser Ile Gly Ala Glu Asp
189          755          760          765
190 Asp Lys Pro Ser Ala Met Asp Val Asp Ser Glu Asn Gly Asn Pro Lys
191      770          775          780
192 Lys Ser Cys Glu Val Gly Glu Arg Glu Gln Trp Cys Leu Ser Thr Leu
193 785          790          795          800
194 Gly Tyr Leu Thr Ala Phe Thr Arg Gln Tyr Ala Ser Glu Ile Trp Pro
195          805          810          815
196 His Met Glu Lys Leu Glu Ser Glu Val Phe Ser Gly Glu Asp Val His
197          820          825          830
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199      835          840          845
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 1250
204 <212> TYPE: DNA
205 <213> ORGANISM: Arabidopsis thaliana
207 <220> FEATURE:
208 <223> OTHER INFORMATION: genomic sequence containing promoter from ABH1
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211 <400> SEQUENCE: 3

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214 gagttaatct ttgacacaag aaacatctct ttctaactctg ttcatagtca aaagaaattg 180
215 tgacaacttc accagatgga agttgtacct ctttattgtt acgaagtgga ttggcgacat 240
216 gaaacaaaaac ccgaacacga acatagtcct gaaactgtga tttttcagag tccatcacca 300
217 cctccttcac ttccccaata cagctcgtga tctctttaat tgtgtcctga gtataatagt 360
218 tcaccgaaat attcctcact cgaccccgaga ttggaagaaa attcagataa tcaattggag 420
219 gattctcaat ccatctatcc atgactacac cccaatttat cttctgtcca aactccaatt 480
220 ttcataattt cttctaaatc ttctcagat ttgaagaaaa attggaatcg atcctttgag 540
221 atagcaacac ctctaaccg agaagaaatt ctccaaattc gtggcatac taatatccaa 600
222 ttagacatcc tttgattctc tagattcaaa aacctaccca actaacgaca gttgtttctg 660
223 ttaattgaac aaaagcgcgg ttgatcagaa agaatcagag gcttattgtc ttaaatcgac 720
224 atattctgaa tggctttatc cagctccatg atgagatcct gatagagagt aaacaacttt 780
225 cccgaactcg tcaaacctga tttgcaggaa acaaaactcca agagaaaaaa cagtgaagaa 840
226 atccgagtaa ttcagatgat aaccaacaca gaactgagaa tcacaaagca aactctcgta 900
227 acagagaaag agtcagaact accaaaaatc cgaggaagaa aacaacaatt tagaccggac 960
228 cgaacacgta aatattttctg gtagaagctc cgttcagaat agaacacctg agagaaaagt 1020
229 ctttaggctc caaattaact gggacgacta ttgttttaac ggctagtttc agctactaag 1080
230 agaaagaaga gagagaaaaa ctttttgtca aactcttttt gtgaactcct tttcttagat 1140
231 gacaacactt atgagaaaaa aaaaaaaaaa ttagttttga cgagacacgg acataaaaaa 1200
232 aaaaactagg gcagagtgac tgataccaaa ggagaaaaca caaagagacg 1250

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235 <210> SEQ ID NO: 4

236 <211> LENGTH: 24

237 <212> TYPE: DNA

238 <213> ORGANISM: Artificial Sequence

240 <220> FEATURE:

241 <223> OTHER INFORMATION: Description of Artificial Sequence: RACE PCR

242 plasmid rescue sequence internal primer

244 <400> SEQUENCE: 4

245 gaagctcaac tcgttgctgg aaag

24

VERIFICATION SUMMARY

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